

Figure 1

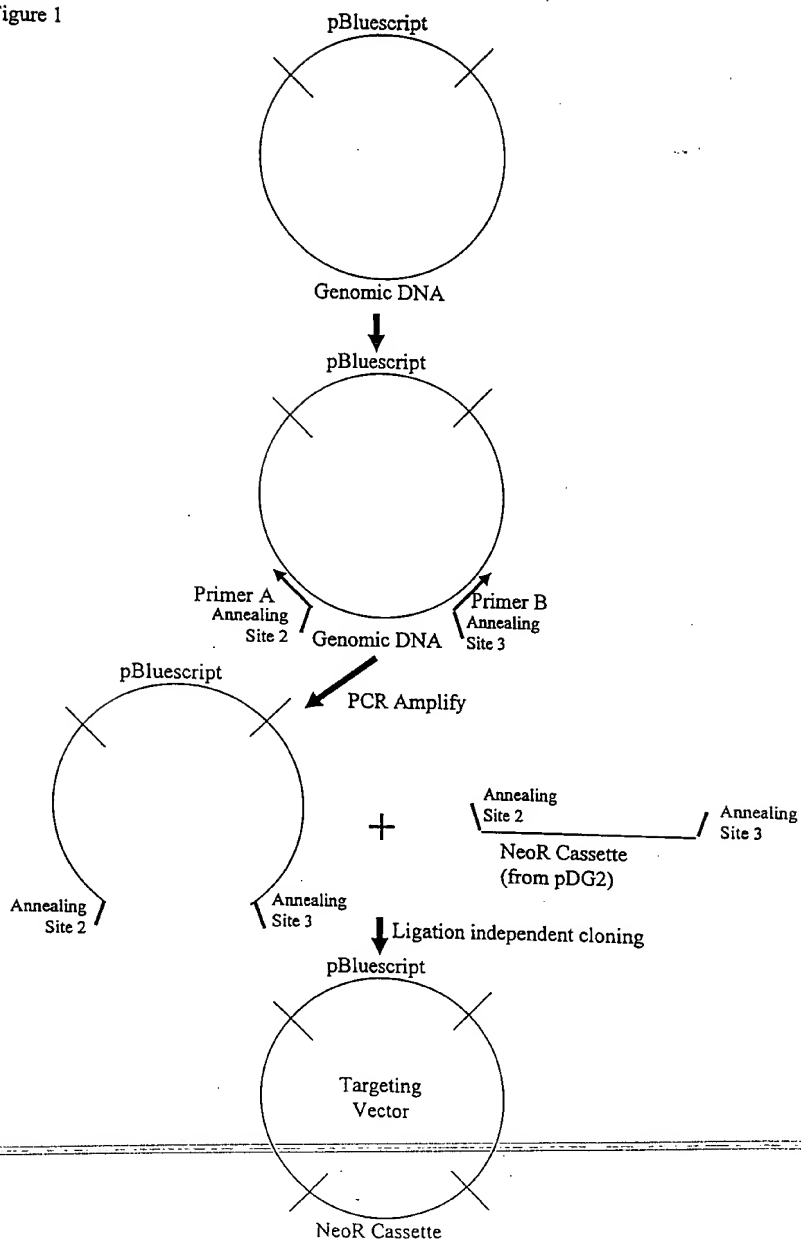
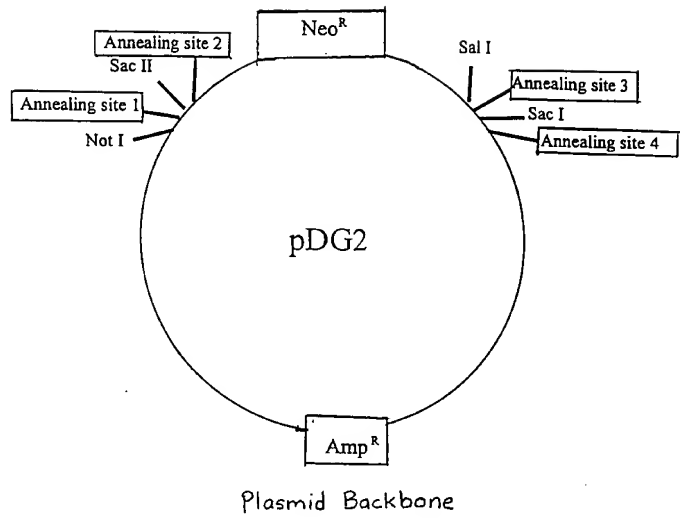


Figure 2A



[illegible]

Fig 2B

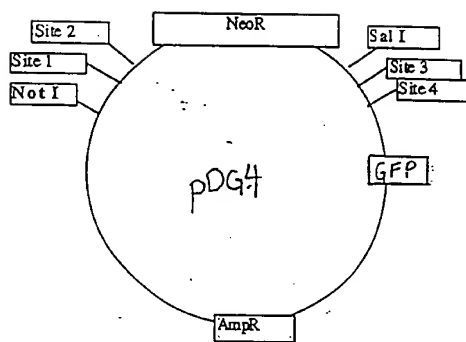


Fig 3A

[illegible]

Fig 3B

Annealing site	Sequence	Sequence after digestion
1	5' tgtgctcctctttggcttgcttcaa... 3' 3' acacgaggagaaaccgaacgaagggt... 5'	5' tgtgctcctctttggcttgcttcaa... 3' 3' tt... 5'
2	5' ctggttcttctgtctggttgcccaa... 3' 3' gaccaagaacagaccgaaccgggtt... 5'	5' ctggttcttctgtctggttgcccaa... 3' 3' tt... 5'
3	5' ggtcctcgctctgtgtccgttgaa... 3' 3' ccaggagcgagacacaggcaactt... 5'	5' ggtcctcgctctgtgtccgttgaa... 3' 3' tt... 5'
4	5' ttgctgtctctgtgtcgtcgaa... 3' 3' aaacgcacaggacacagcagctt... 5'	5' ttgctgtctctgtgtcgtcgaa... 3' 3' tt... 5'

Fig 4

Annealing site	Sequence	Sequence after digestion
1	5' AAtgtgctcctcttttggttgettCOGC 3' 3' Ttacacgaggagaaaccgaacgaagg 5'	5' AA 3' 3' Ttacacgaggagaaaccgaacgaagg 5'
2	5' AActggttcttctgtctggttggcCOGC 3' 3' Ttgaccaagaacagaccgaaccggg 5'	5' AA 3' 3' Ttgaccaagaacagaccgaaccggg 5'
3	5' AAggtcctcgctctgtgtccgttGAGCT 3' 3' Ttccaggagcgagacacaggcaac 5'	5' AA 3' 3' Ttccaggagcgagacacaggcaac 5'
4	5' AAttgcgtgtcctgtgtcgtcGAGCT 3' 3' Ttaaacgcacaggacacagcagc 5'	5' AA 3' 3' Ttaaacgcacaggacacagcagc 5'

Fig 5

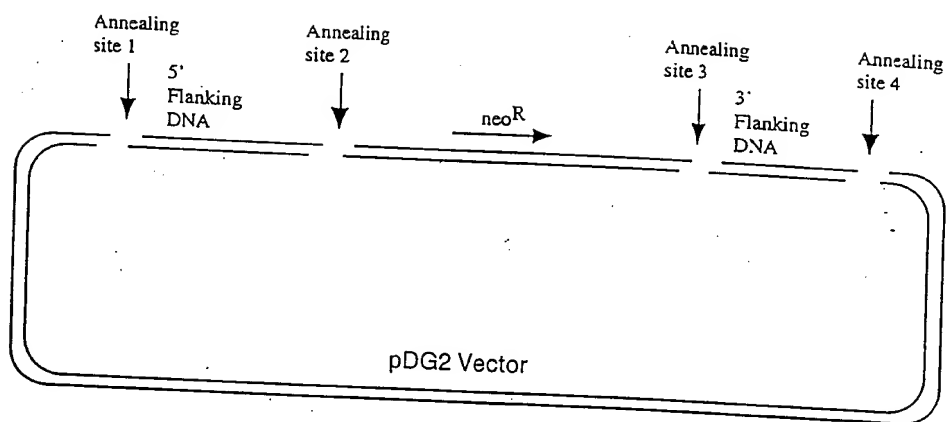


Fig 6

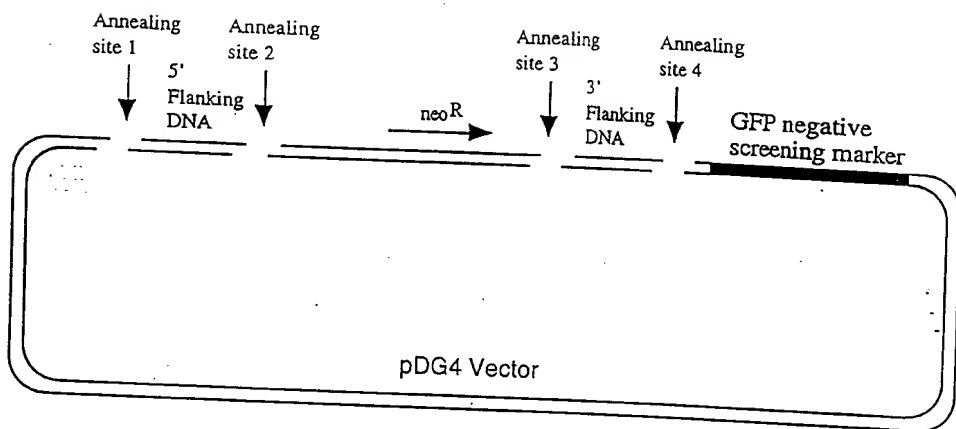


Fig 7

Oligo#	Sequence (5' to 3')
174	ATGACCGCTCAGGAAACCTGTTGCA
180	ATAGGCATAGTAGGCCAGCTTGAGG
454	tgtgctcctctttggcttgcttccAATTAAACCCTCACTAAAGGGAACGAAT
463	ctgggtctctgtctggcttggcccaaTGCAACAGGTTTCTGAGCGGTCAAT
464	ggtcctcgctctgtgtccgttgaaCCTCAAGCTGGCCTACTATGCCTAT
42	tttgcggtgctctgtgtcgtagaaCGACTAATACGACTCACTATAGGGCG
151	GCCAATGGACTCTTAGTTTGGAAAC
155	GTTCTGGCAACAAATTCGGCGCAC
454	tgtgctcctctttggcttgcttccAATTAAACCCTCACTAAAGGGAACGAAT
465	ctgggtctctgtctggcttggcccaaGTTCCAAACTAAGAGTCCATTGGC
466	ggtcctcgctctgtgtccgttgaaGTGCGCGGAATTTGTTTGCCAGAAC
1	GAACCTTGGTGTGCCAAGTTACTTC
2	GAACCTTGGCTGAACCCCTTGTCT
41	tgtgctcctctttggcttgcttgaCGACTAATACGACTCACTATAGGGCG
38	ctgggtctctgtctggcttggcccaaGAAGTAACCTTGGCACACCAAGGTTC
40	ggtcctcgctctgtgtccgttgaaAGAACAAAGGGTTTCAGCCAAAGTTC
37	tttgcggtgctctgtgtcgtagAATTAAACCCTCACTAAAGGGAACGAAT
540	ATGCCGGATCTCCTACTACTGGGCC
546	TGTCATAGTAGACAGCGATGGAACG
445	GACAAGAACCAGTTGACGTCAAGCTTCCCGGGACGCGTCTAGCGGCGCGCCG
667	ctgggtctctgtctggcttggcccaaGGCCAGTAGTAGGAGATCCGGCAT
668	ggtcctcgctctgtgtccgttgaaCGTTCATCGCTGTCTACTATGACA
907	ctgggtctctgtctggcttggcccaaAAAGCCGACAGCCAGCTCACAAGC
908	ggtcctcgctctgtgtccgttgaaGCCCAATGCCACAGAGACAGAATGT
1157	ctgggtctctgtctggcttggcccaaGTTGGATCCTCTCCAAGGCCCCATCT
1158	ggtcctcgctctgtgtccgttgaaCTCCAGTGCCGAGTGTGTGGGGACAG

Figure 8